

SEQUENCE LISTING

(1) GENERAL INFORMATION

- 9220X
- (i) APPLICANT: Morrison, Sherie L.
Chintalacharuvu, Kote R.
- (ii) TITLE OF THE INVENTION: SECRETORY IMMUNOGLOBULIN PRODUCED
BY SINGLE CELLS AND METHODS FOR MAKING AND USING
SAME
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
(B) STREET: 11150 Santa Monica Boulevard, Suite 400
(C) CITY: Los Angeles
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 90025
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 09-JUN-1998
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/050,969
(B) FILING DATE: 19-JUN-1997
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Canady, Karen S
(B) REGISTRATION NUMBER: 39,927
(C) REFERENCE/DOCKET NUMBER: 30435.45USU1
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 310 445-1140
(B) TELEFAX: 310 445-9031
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGGCAGAACG GTGACCATCA ACTGCCCTTT

30

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AAGGAATTCC TACTCTGCAA AAAGCCTGGG GTCCTGAATG GC

42

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1839 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGCTGCTCT	TCGTGCTCAC	CTGCCTGCTG	GCGGTCTTCC	CAGCCATCTC	CACGAAGAGT	60
CCCATATTTG	GTCCCGAGGA	GGTGAATAGT	GTGGAAGGTA	ACTCAGTGTC	CATCACGTGC	120
TACTACCCAC	CCACCTCTGT	CAACCGGCAC	ACCCGGAAGT	ACTGGTGCCG	GCAGGGAGCT	180
AGAGGTGGCT	GCATAACCCT	CATCTCCTCG	GAGGGCTACG	TCTCCAGCAA	ATATGCAGGC	240
AGGGCTAACC	TCACCAACTT	CCCGGAGAAC	GGCACATTTG	TGGTGAACAT	TGCCCAGCTG	300
AGCCAGGATG	ACTCCGGGCG	CTACAAGTGT	GGCCTGGGCA	TCAATAGCCG	AGGCCGTGCC	360
TTTGATGTCA	GCCTGGAGGT	CAGCCAGGGT	CCTGGGCTCC	TAAATGACAC	TAAAGTCTAC	420
ACAGTGGACC	TGGGCAGAAC	GGTGACCATC	AACTGCCCTT	TCAAGACTGA	GAATGCTCAA	480
AAGAGGAAGT	CCTTGATACAA	GCAGATAGGC	CTGTACCCTG	TGCTGGTCAT	CGACTCCAGT	540
GGTTATGTGA	ATCCCAACTA	TACAGGAAGA	ATACGCCTTG	ATATTCAGGG	TACTGGCCAG	600
TTACTGTTCA	GCGTTGTCAT	CAACCAACTC	AGGCTCAGCG	ATGCTGGGCA	GTATCTCTGC	660
CAGGCTGGGG	ATGATTCCAA	TAGTAATAAG	AAGAATGCTG	ACCTCCAAGT	GCTAAAGCCC	720
GAGCCCGAGC	TGGTTTATGA	AGACCTGAGG	GGCTCAGTGA	CCTTCCACTG	TGCCCCTGGG	780
CCTGAGGTGG	CAAACGTGGC	CAAATTTCTG	TGCCGACAGA	GCAGTGGGGA	AAACTGTGAC	840
GTGGTCGTCA	ACACCCTGGG	GAAGAGGGCC	CCAGCCTTTG	AGGGCAGGAT	CCTGCTCAAC	900
CCCCAGGACA	AGGATGGCTC	ATTCAGTGTG	GTGATCACAG	GCCTGAGGAA	GGAGGATGCA	960
GGGCGCTACC	TGTGTGGAGC	CCATTCGGAT	GGTCAGCTGC	AGGAAGGCTC	GCCTATCCAG	1020
GCCTGGCAAC	TCTTCGTCAA	TGAGGAGTCC	ACGATTCCCC	GCAGCCCCAC	TGTGGTGAAG	1080
GGGGTGGCAG	GAAGCTCTGT	GGCCGTGCTC	TGCCCCTACA	ACCGTAAGGA	AAGCAAAAGC	1140
ATCAAGTACT	GGTGTCTCTG	GGAAGGGGCC	CAGAATGGCC	GCTGCCCCCT	GCTGGTGGAC	1200
AGCGAGGGGT	GGGTTAAGGC	CCAGTACGAG	GGCCGCCTCT	CCCTGCTGGA	GGAGCCAGGC	1260
AACGGCACCT	TCACTGTCAT	CCTCAACCAG	CTCACCAGCG	GGGACGCCGG	CTTCTACTGG	1320
TGTCTGACCA	ACGGCGATAC	TCTCTGGAGG	ACCACCGTGG	AGATCAAGAT	TATCGAAGGA	1380
GAACCAAAAC	TCAAGGTACC	AGGGAATGTC	ACGGCTGTGC	TGGGAGAGAC	TCTCAAGGTC	1440
CCCTGTCACT	TTCCATGCAA	ATTCTCCTCG	TACGAGAAAT	ACTGGTGCAA	GTGGAATAAC	1500
ACGGGCTGCC	AGGCCCTGCC	CAGCCAAGAC	GAAGGCCCCA	GCAAGGCCTT	CGTGAAGTGT	1560
GACGAGAACA	GCCGGCTTGT	CTCCCTGACC	CTGAACCTGG	TGACCAGGGC	TGATGAGGGC	1620
TGGTACTGGT	GTGGAGTGAA	GCAGGGCCAC	TTCTATGGAG	AGACTGCAGC	CGTCTATGTG	1680
GCAGTTGAAG	AGAGGAAGGC	AGCGGGGTCC	CGCGATGTCA	GCCTAGCGAA	GGCAGACGCT	1740
GCTCCTGATG	AGAAGGTGCT	AGACTCTGGT	TTTCGGGAGA	TTGAGAACAA	AGCCATTTCAG	1800
GATCCCAGGC	TTTTTGCAGA	GTAGGAATTC	CTGCAGCCC			1839

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Leu	Leu	Phe	Val	Leu	Thr	Cys	Leu	Leu	Ala	Val	Phe	Pro	Ala	Ile
1				5					10					15	
Ser	Thr	Lys	Ser	Pro	Ile	Phe	Gly	Pro	Glu	Glu	Val	Asn	Ser	Val	Glu
			20					25					30		
Gly	Asn	Ser	Val	Ser	Ile	Thr	Cys	Tyr	Tyr	Pro	Pro	Thr	Ser	Val	Asn
			35				40					45			
Arg	His	Thr	Arg	Lys	Tyr	Trp	Cys	Arg	Gln	Gly	Ala	Arg	Gly	Gly	Cys
	50					55					60				
Ile	Thr	Leu	Ile	Ser	Ser	Glu	Gly	Tyr	Val	Ser	Ser	Lys	Tyr	Ala	Gly
65					70					75					80
Arg	Ala	Asn	Leu	Thr	Asn	Phe	Pro	Glu	Asn	Gly	Thr	Phe	Val	Val	Asn
				85					90					95	
Ile	Ala	Gln	Leu	Ser	Gln	Asp	Asp	Ser	Gly	Arg	Tyr	Lys	Cys	Gly	Leu
			100					105					110		
Gly	Ile	Asn	Ser	Arg	Gly	Leu	Ser	Phe	Asp	Val	Ser	Leu	Glu	Val	Ser
		115					120					125			
Gln	Gly	Pro	Gly	Leu	Leu	Asn	Asp	Thr	Lys	Val	Tyr	Thr	Val	Asp	Leu
		130				135					140				
Gly	Arg	Thr	Val	Thr	Ile	Asn	Cys	Pro	Phe	Lys	Thr	Glu	Asn	Ala	Gln
145					150					155					160
Lys	Arg	Lys	Ser	Leu	Tyr	Lys	Gln	Ile	Gly	Leu	Tyr	Pro	Val	Leu	Val
				165					170					175	
Ile	Asp	Ser	Ser	Gly	Tyr	Val	Asn	Pro	Asn	Tyr	Thr	Gly	Arg	Ile	Arg
			180					185					190		
Leu	Asp	Ile	Gln	Gly	Thr	Gly	Gln	Leu	Leu	Phe	Ser	Val	Val	Ile	Asn
		195					200					205			
Gln	Leu	Arg	Leu	Ser	Asp	Ala	Gly	Gln	Tyr	Leu	Cys	Gln	Ala	Gly	Asp
		210				215					220				
Asp	Ser	Asn	Ser	Asn	Lys	Lys	Asn	Ala	Asp	Leu	Gln	Val	Leu	Lys	Pro
225					230					235					240
Glu	Pro	Glu	Leu	Val	Tyr	Glu	Asp	Leu	Arg	Gly	Ser	Val	Thr	Phe	His
				245					250					255	
Cys	Ala	Leu	Gly	Pro	Glu	Val	Ala	Asn	Val	Ala	Lys	Phe	Leu	Cys	Arg
			260					265					270		
Gln	Ser	Ser	Gly	Glu	Asn	Cys	Asp	Val	Val	Val	Asn	Thr	Leu	Gly	Lys
		275					280					285			
Arg	Ala	Pro	Ala	Phe	Glu	Gly	Arg	Ile	Leu	Leu	Asn	Pro	Gln	Asp	Lys
		290				295					300				
Asp	Gly	Ser	Phe	Ser	Val	Ile	Thr	Gly	Leu	Arg	Lys	Glu	Asp	Ala	
305					310				315					320	
Gly	Arg	Tyr	Leu	Cys	Gly	Ala	His	Ser	Asp	Gly	Gln	Leu	Gln	Glu	Gly
				325					330					335	
Ser	Pro	Ile	Gln	Ala	Trp	Gln	Leu	Phe	Val	Asn	Glu	Glu	Ser	Thr	Ile
			340					345					350		
Pro	Arg	Ser	Pro	Thr	Val	Val	Lys	Gly	Val	Ala	Gly	Ser	Ser	Val	Ala
		355					360					365			
Val	Leu	Cys	Pro	Tyr	Asn	Arg	Lys	Glu	Ser	Lys	Ser	Ile	Lys	Tyr	Trp
		370				375					380				

Cys	Leu	Trp	Glu	Gly	Ala	Gln	Asn	Gly	Arg	Cys	Pro	Leu	Leu	Val	Asp
385					390					395					400
Ser	Glu	Gly	Trp	Val	Lys	Ala	Gln	Tyr	Glu	Gly	Arg	Leu	Ser	Leu	Leu
				405					410						415
Glu	Glu	Pro	Gly	Asn	Gly	Thr	Phe	Thr	Val	Ile	Leu	Asn	Gln	Leu	Thr
			420					425					430		
Ser	Arg	Asp	Ala	Gly	Phe	Tyr	Trp	Cys	Leu	Thr	Asn	Gly	Asp	Thr	Leu
		435					440					445			
Trp	Arg	Thr	Thr	Val	Glu	Ile	Lys	Ile	Ile	Glu	Gly	Glu	Pro	Asn	Leu
	450					455					460				
Lys	Val	Pro	Gly	Asn	Val	Thr	Ala	Val	Leu	Gly	Glu	Thr	Leu	Lys	Val
465					470					475					480
Pro	Cys	His	Phe	Pro	Cys	Lys	Phe	Ser	Ser	Tyr	Glu	Lys	Tyr	Trp	Cys
				485					490					495	
Lys	Trp	Asn	Asn	Thr	Gly	Cys	Gln	Ala	Leu	Pro	Ser	Gln	Asp	Glu	Gly
		500						505					510		
Pro	Ser	Lys	Ala	Phe	Val	Asn	Cys	Asp	Glu	Asn	Ser	Arg	Leu	Val	Ser
		515					520					525			
Leu	Thr	Leu	Asn	Leu	Val	Thr	Arg	Ala	Asp	Glu	Gly	Trp	Tyr	Trp	Cys
	530					535					540				
Gly	Val	Lys	Gln	Gly	His	Phe	Tyr	Gly	Glu	Thr	Ala	Ala	Val	Tyr	Val
545					550					555					560
Ala	Val	Glu	Glu	Arg	Lys	Ala	Ala	Gly	Ser	Arg	Asp	Val	Ser	Leu	Ala
				565					570					575	
Lys	Ala	Asp	Ala	Ala	Pro	Asp	Glu	Lys	Val	Leu	Asp	Ser	Gly	Phe	Arg
			580					585					590		
Glu	Ile	Glu	Asn	Lys	Ala	Ile	Gln	Asp	Pro	Arg	Leu	Phe	Ala	Glu	Glx
		595					600					605			

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